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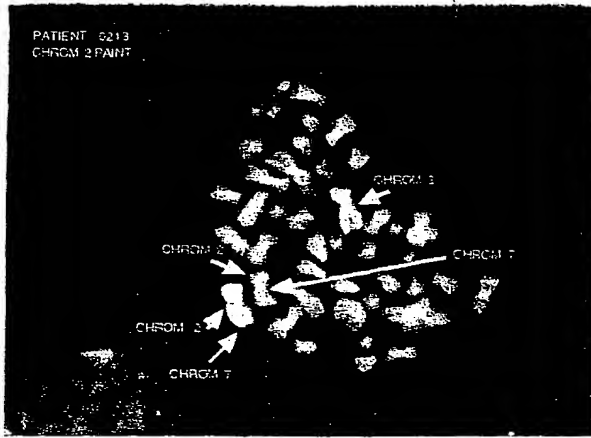


FIGURE 1A

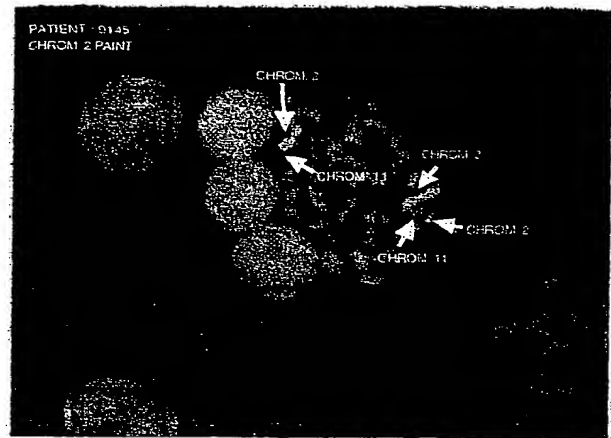


FIGURE 1B

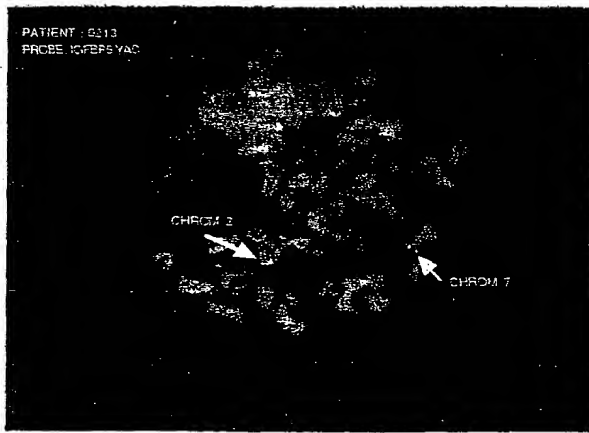


FIGURE 2A



FIGURE 2B

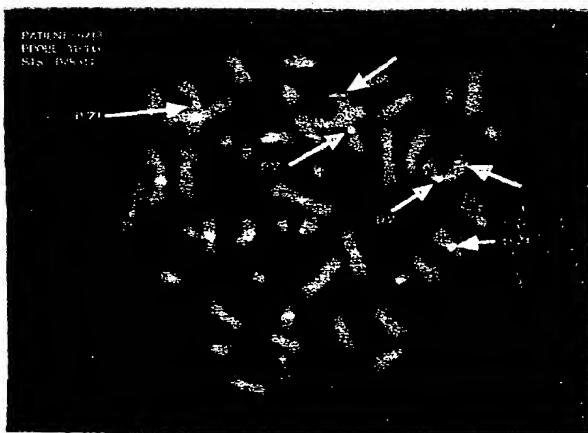


FIGURE 3A

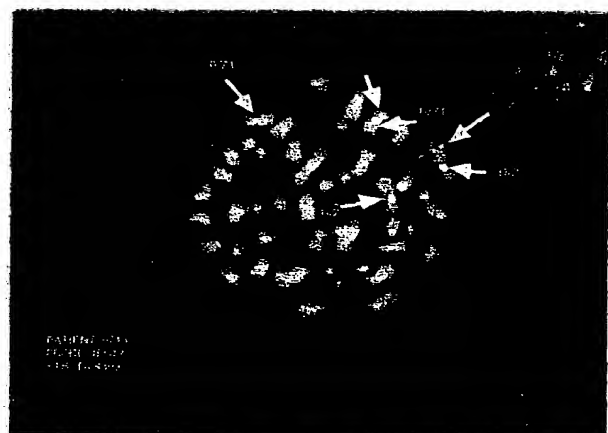
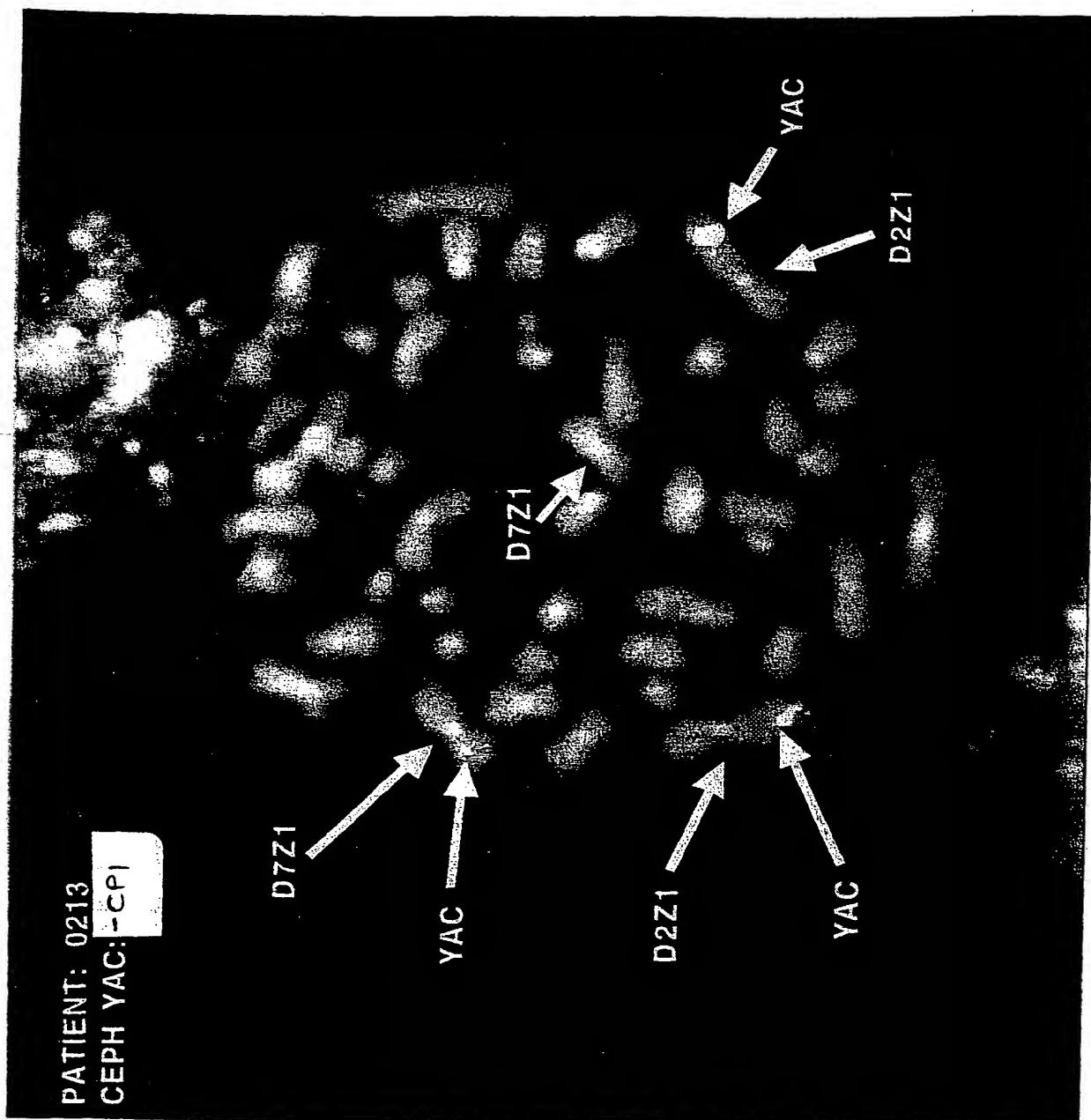


FIGURE 3B

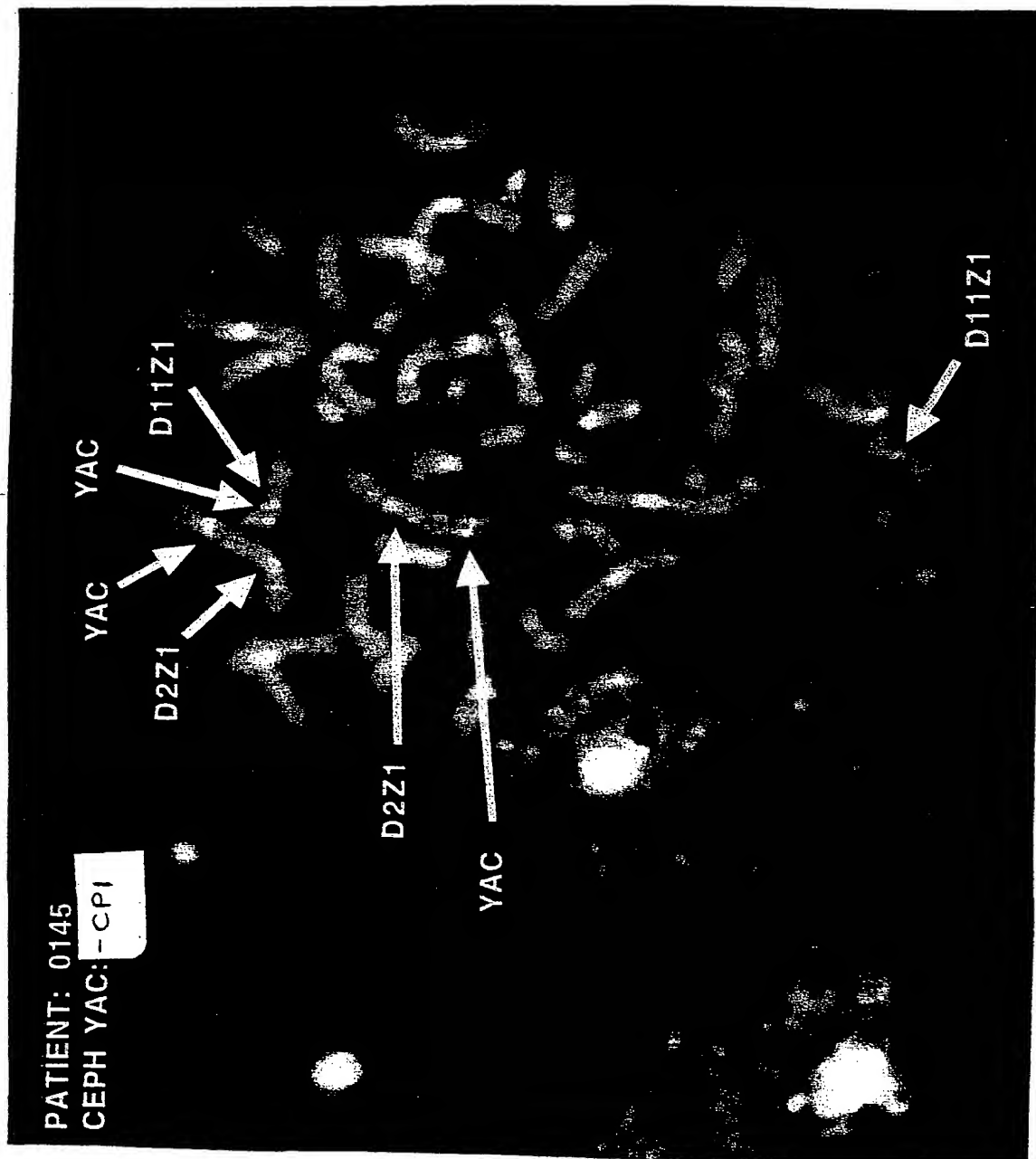
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Figure 4



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Figure 5



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FIGURE 6

SEQ ID NO:1 (Human cDNA)

3 ggaggattcgcagttcaacatcaagggtccctgtgcgtttttattgcgacctgccgggtggga
63 actttgtctccgagtcggagcagcatggagcggcggagcgcagagcccgtgtctgcgggac
M E R R S E S P C L R D
123 agccccgaccggcggagcggcagcccgacgtcaaggggcctccccagtgaaaggtggcc
S P D R R S G S P D V K G P P P V K V A
183 cggctggagcagaacggcagccccatggagcccgcgaggcccaacggcgccgtggcc
R L E Q N G S P M G A R G R P N G A V A
243 aaggccgtgggaggtttgatgattcctgtcttttctgtcgtggagcagttggacggtct
K A V G G L M I P V F C V V E Q L D G S
303 cttgaatacgacaacagagaagaacacgccgagtttgcctggtgcggaaagatgtgctt
L E Y D N R E E H A E F V L V R K D V L
363 tttagccagctggtggagactgcgctcctggccctggggattctcacagctctgcggcc
F S Q L V E T A L L A L G Y S H S S A A
423 caggcccaaggaataataagctgggaaggtggaaccctctccccctcagttatgtgaca
Q A Q G I I K L G R W N P L P L S Y V T
483 gatgcacccgacgcgacagtggccgacatgctacaagatgtctatcatgttgtagcttg
D A P D A T V A D M L Q D V Y H V V T L
543 aaaatccaattacaaagttgttcaaagttggaagacttgctgcggagcagtggaaccat
K I Q L Q S C S K L E D L P A E Q W N H
603 gccacagtccgcaatgccttaaggaactgctcaaagagatgaaccagagcacattagcc
A T V R N A L K E L L K E M N Q S T L A
663 aaagaatgccctctctcccagagtatgatttcatccattgtaaatagcacatattatgcc
K E C P L S S Q S M I S S I V N S T Y Y A
723 aatgtgtcagcaaccaagtgccaggagttgggagatggtataaaaagtacaagaagatt
N V S A T K C Q E F G R W Y K K Y K I
783 aaagtggaaagagtggaaacgagaaaaacctttcagactattgtgttctgggcagcgcca
K V E R V E R E N L S D Y C V L G Q R P
843 atgcatttaccaaataatgaaccagctggcatccctggggaaaaccaacgaacagtctcct
M H L P N M N Q L A S L G K T N E Q S P
903 cacagccaaattcaccacagtaactccaatccgaaaccaagtgccgcattacagcccatc
H S Q I H H S T P I R N Q V P A L Q P I
963 atgagccctgggtcttctttctcccagcttagtccacaacttgtaaggcaacaaatagcc
M S P G L L S P Q L S P Q L V R Q Q I A
1023 atggcccatctgataaaccaacagattgccgttagccggctcctggctcaccagcatcct
M A H L I N Q Q I A V S R L L A H Q H P
1083 caagccatcaaccagcagttcctgaaccatccaccatccccagagcagtttagccagag
Q A I N Q Q F L N H P P I P R A V K P E
1143 ccaaccaactcttccgtggaagtctctccagatatctaccagcaagtcagagatgagctg
P T N S S V E V S P D I Y Q Q V R D E L
1203 aagagggccagtggtgtcccaagctgtctttgcaagagtggcattcaaccgcacacagggg
K R A S V S Q A V F A R V A F N R T Q G
1263 ttgttgtctgagattctgcgtaaggaagaagacctcggacagcctctcagttcttcta
L L S E I L R K E E D P R T A S Q S L L
1323 gtaaacctgagggccatgcagaatttctcaatctgccagaagtggagcgcagatcgcac
V N L R A M Q Q N F L N L P E V E R D R I
1383 taccaggtatgagagggagcggagcgaatcccaatgtgagcatggtctcctcggccctcc
Y Q D E R E R S M N P N V S M V S S A S
1443 agcagtcaccagctcctccgaacccctcaggccaaaacctcgacaccgacaacagacctc
S S P S S S R T P Q A K T S T P T T D L
1503 cctattaaggtggacggcgccaacatcaacatcacagctgccatttatgacgagatccaa
P I K V D G A N I N I T A A I Y D E I Q
1563 caggagatgaaaagggccaaggtgtctcaagccctgtttgccaaagtggctgcaaataaa
Q E M K R A K V S Q A L F A K V A A N K

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1623 agtcaggsgctggctgtgtgaactgctccgctggaaggagaacccaagcccagaaaaaccgc
S Q G W L C E L L R W K E N P S P E N R
1683 accctctgggaaaacctctgtaccatccgtcgcttccctgaaccttccccagcatgagagg
T L W E N L C T I R R F L N L P Q H E R
1743 gatgtcatctatgaggaggagtgcaaggcatcaccacagcgaacgcatgcaacacgtggtc
D V I Y E E E S R H H H S E R M Q H V V
1803 cagcttccccctgagccgggtgcaggctacttcatagacagcagtcctcagccagccaaggag
Q L P P E P V Q V L H R Q Q S Q P A K E
1863 agttccccctcccagagaagaagcgccctccccacctcctccgactgaagacagttgtgcc
S S P P R E E A P P P P P P T E D S C A
1923 aaaaagccccgggtctcgcacaaagatctccttagaagccctggggatcctccaaagcttt
K K P R S R T K I S L E A L G I L Q S F
1983 attcatgatgtaggcctgtaccagaccaggaagccatccacactctttcggctcagctg
I H D V G L Y P D Q E A I H T L S A Q L
2043 gatctcccaaacacaccatcatcaagttcttccagaaccagcggtaccacgtgaagcac
D L P K H T I I K F F Q N Q R Y H V K H
2103 caggggaagctgaaagagcacctgggctccgcggtggacgtggctgaatataaggacgag
H G K L K E H L G S A V D V A E Y K D E
2163 gagctgctgaccgagtcagaggagaaacgacagcgagggaaggctccgaggagatgtacaaa
E L L T E S E E N D S E E G S E E M Y K
2223 gtggaggctgaggaggaaaaatgctgacaaaagcaaggcagcacctgccgaaattgaccag
V E A E E E N A D K S K A A P A E I D Q
2283 agataatgtgaacttctactaggcaaagcaatacatcggtccaaggattttctgctttca
R *
2343 tttctttaaaagtttttgttagtttgtttttgtttttgtttttgggttttttggctt
2403 tatttttgtctttttatgtctgttttgtttttcttacccttttggacatttctttgttgc
2463 acaggatacacctatagactgaataagttcagtatttccgaatcagacatcgcccttggca
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2643 ggatgaaaagaactatgaaataaatgaaggaagctacaagtgtgtgtgtatatgtatatg
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2763 cgaaagaatagactgtgaaatgagttcttaagaaaaagacttgtttatgtattaaaaaaa
2823 ccacttcacagtgagtcgctttggctttttgataaaactgoggcctgctctcaggggtgggg
2883 tgactattcttgaattcctattttactttttgtgtttgtccctgatttttttttaattc
2943 tatggcttcctatctggcagcttaatgggtaatttttgagggtatgtatttaacaaaataa
3003 acgacactgccgaaaaaaaaaaaaagtggaagtgaaaacaatcagggcacattaaaatgata
3063 caagtcaaataaatcttaaagacacaatgcacacttaaaatgactcaataaaatgacttg
3123 ctacgttccggttattcaatttgtcattactgtagtgaacagatgcatttctgtggaattc
3183 caaataagtaaaaactgaaattcagtgagagaaaaactttgtccactagtgcaagctctga
3243 tcaaatgacattttgacattggacatatggaattcatagtatgagccacattttgtgtg
3303 aaattttatttacctgcttgtggcttcaaactctgaaaattaataagcctgctcgtttaaaa

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3363 gttgtttgttgttgcgtgttttttgccttttgccttttactagaaaaatagttcagtgta
3423 atattaagttagaaaagaagttgctgcccagttaaaggggctccctctcaaataaatctc
3483 catccttccctctcccaaaagacatttctgatttctgcttcactttgggcttccctctct
3543 tcgtacacattccatctacctaatacaaacattttcagtccttgatctctctctgtccctt
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3663 gagtatgtgaagcgatttcagtagaatcacttactcatcctaaaagaaaacattatccca
3723 gttacctacatcgcaattaccttatgtaaagcagaactaatgctgactggatgtttaatg
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3843 gaaacaccagaagcattactttccacttctacttacagtaattgcaagaggagacctcac
3903 attcaggactggcctagtgaacgtaataccatgctttaaactggccattaaacagtcccac
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4083 taatactatttatatatttgaaagggtataaaaggtaggagttaaaaaaaaaacctctatg
4143 tgtagatattaactcagaacttacaatataggggagaagacatgttgcaatacaagcta
4203 attctagctgctcagtaacctctggagtttttaaagggaacattttcctgtacttttcaa
4263 ataatgatgtttaaaaattatcttgacataagcgatataacctttgcaaaaggatgggt
4323 gtttgcagtttagccctggcccatccttctctatttctgtagtagtgcagctttaatca
4383 gaaagtccatgggtgctgcttccctgatctccgagttactctttccaaattgtcttcttac
4443 actgttgctgaagggtcactctgtacacgtaatggaaaactgattttgccaagctcttaca
4503 ggtgggttcactctatcgatggcatccgcatttgggtatcttttacacttcaacaaaaattt
4563 attaggtatttttcaatgctaagtcctgccttttattttttaatttcactgccaagtttg
4623 cagtgggttctaagtgaatctgtgggcatttttagcctgtgggtcttgccagatctttgcgaa
4683 ttacaatgcatatatgtctatttatccaatatctgtcatataatatctatttggaagaag
4743 aaactttctcttgtagtgccctcttgacaaaagcacaatttcccgccctttttttttttt
4803 gtgaaatgaaaaaaacaaattgtgtttattgcggtatcaacaatgtgaataaggattaa
4863 catattgtaaatgttcttttttccatgtaaatcaactatctttgttatcactaagtgata
4923 attaattttaacttatgtgcattgtaggctgttagaatttttgggtgttaaaaataaa
4983 cgcattcaataaatatg 4999

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FIGURE 7 SEQ ID NO:2 (Human amino acid sequence)

87 atggagcgggcgagcgagagcccgtgtctgcgggacagccccgac
M E R R S E S P C L R D S P D
132 cggcggagcgggcagccccgacgtcaaggggctccccagtgaaag
R R S G S P D V K G P P P V K
177 gtggccccggctggagcagaacggcagccccatgggagccccggg
V A R L E Q N G S P M G A R G
222 aggcccaacggcgccgtggccaaggccgtgggaggtttgatgatt
R P N G A V A K A V G G L M I
267 cctgtcttttgtgtcgtggagcagttggacggctctcttgaatat
P V F C V V E Q L D G S L E Y
312 gacaacagagaagaacacgcccagtttgcctgggtgcggaagat
D N R E E H A E F V L V R K D
357 gtgcttttttagccagctgggtggagactgcgctcctggccctggg
V L F S Q L V E T A L L A L G
402 tattctcacagctctgcgggccagggcccaaggaataatcaagctg
Y S H S S A A Q A Q G I I K L
447 ggaaggtggaaccctctccccctcagttatgtgacagatgcaccc
G R W N P L P L S Y V T D A P
492 gacgcgacagtgggcgacatgctacaagatgtctatcatgttgtg
D A T V A D M L Q D V Y H V V
537 acgttgaaaatccaattacaaagtgttcaaagttggaagacttg
T L K I Q L Q S C S K L E D L
582 cctgcgagcagtggaaccatgccacagtcgcgaatgccttaaag
P A E Q W N H A T V R N A L K
627 gaactgctcaaagagatgaaccagagcacattagccaaagaatgc
E L L K E M N Q S T L A K E C
672 cctctctcccagagtatgatttcattccattgtaaatagcacatat
P L S Q S M I S S I V N S T Y
717 tatgccaatgtgtcagcaaccaagtgcaggagtttgggagatgg
Y A N V S A T K C Q E F G R W
762 tataaaaagtacaagaagattaaagtggaaagagtggaacgagaa
Y K K Y K K I K V E R V E R E
807 aacctttcagactattgtgttctggggccagcgtccaatgcattta
N L S D Y C V L G Q R P M H L
852 ccaaatatgaaccagctggcatccctggggaaaaccaacgaacag
P N M N Q L A S L G K T N E Q
897 tctcctcacagccaaattcaccacagtactccaatccgaaaccaa
S P H S Q I H H S T P I R N Q
942 gtgcccgcattacagcccatcatgagccctgggtcttcttctccc
V P A L Q P I M S P G L L S P
987 cagcttagtccacaacttgtaaggcaacaaatagccatggcccat
Q L S P Q L V R Q Q I A M A H
1032 ctgataaaccaacagattgccgttagccggctcctgggtcaccag
L I N Q Q I A V S R L L A H Q
1077 catcctcaagccatcaaccagcagttcctgaaccatccacccatc
H P Q A I N Q Q F L N H P P I
1122 cccagagcagtttaagccagagccaaccaactcttcctggaagtc
P R A V K P E P T N S S V E V
1167 tctccagatatctaccagcaagtccagagatgagctgaagagggcc
S P D I Y Q Q V R D E L K R A
1212 agtgtgtcccaagctgtctttgcaagagtggcattcaaccgcaca
S V S Q A V F A R V A F N R T
1257 cagggattgtgtctgagattctgcgtaaggaagaagaccctcgg
Q G L S E I L R K E E D P R
1302 acagcctctcagttctcttctagtaaacctgagggccatgcagaat
T A S Q S L L V N L R A M Q N

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1347 ttccctcaatctgccagaagtggagcgagatcgcatctaccaggat
F L N L P E V E R D R I Y Q D
1392 gagagggagcgggagcatgaatcccaatgtgagcatggtctcctcg
E R E R S M N P N V S M V S S
1437 gccctccagcagtcgccagctcctcccgaaacctcaggccaaaacc
A S S S P S S S R T P Q A K T
1482 tcgacaccgacaacagacacctccctattaaggtggacggcgccaac
S T P T T D L P I K V D G A N
1527 atcaacatcacagctgccatttatgacgagatccaacaggagatg
I N I T A A I Y D E I Q Q E M
1572 aaaagggccaaggtgtctcaagccctgtttgcaaagtggctgca
K R A K V S Q A L F A K V A A
1617 aataaaagtccagggtgtgtgtgaactgctccgctggaaggag
N K S Q G W L C E L L R W K E
1662 aacccaagcccagaaaaccgcacctctgtgggaaaacctctgtacc
N P S P E N R T L W E N L C T
1707 atccgtcgcttctcctgaaccttccccagcatgagagggatgtcatc
I R R F L N L P Q H E R D V I
1752 tatgaggaggagtcaaggcatcaccacagcgaacgcacatgcaacac
Y E E S R H H H S E R M Q H
1797 gtggtccagcttccccctgagccggtgcagggtacttcatagacag
V V Q L P P E P V Q V L H R Q
1842 cagtctcagccagccaaggagagttccccctcccagagaagaagcg
Q S Q P A K E S S P P R E E A
1887 cctccccacctcctccgactgaagacagttgtgccaaaaagccc
P P P P P P T E D S C A K K P
1932 cggctctcgacaaaagatctccttagaagccctggggatcctccaa
R S R T K I S L E A L G I L Q
1977 agctttattcatgatgtaggcctgtacccagaccaggaagccatc
S F I H D V G L Y P D Q E A I
2022 cacactctttcggctcagctggatctccccaacacaccatcatc
H T L S A Q L D L P K H T I I
2067 aagttcttccagaaccagcgggtaccacgtgaagcaccacgggaag
K F F Q N Q R Y H V K H H G K
2112 ctgaaagagcacctgggctccgcggtggacgtggctgaatataag
L K E H L G S A V D V A E Y K
2157 gacgaggagctgctgaccgagtcagaggagaacgacagcgaggaa
D E E L L T E S E E N D S E E
2202 ggctccgaggagatgtacaaagtggaggctgaggaggaaaatgct
G S E E M Y K V E A E E E N A
2247 gacaaaagcaaggcagcacctgccgaaattgaccagagataa 2288
D K S K A A P A E I D Q R *

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FIGURE 8

SEQ ID NO 3 (Mouse cDNA)

1 atggagcggcgagcgcgagagcccgtgtcttcgggacagccccgac
M E R R S E S P C L R D S P D
46 cgaagaagcggcagcccygacgtcaagggcctcccccggtgaag
R R S G S P D V K G P P P V K
91 gtggccccggtggagcagaacggcagccccatgggagcccgcg
V A R L E Q N G S P M G A R G
136 aggcccaacggcgccgtggccaaggccgtgggaggtttgatgatt
R P N G A V A K A V G G L M I
181 ccagttttctgtgtggtggagcagttggatggctctcttgaatac
P V F C V V E Q L D G S L E Y
226 gacaaccgagaagagcacgctgagttcgtcttggtgcggaaagat
D N R E E H A E F V L V R K D
271 gtgcttttttagccagctggtggagaccgcgctcctggccctggg
V L F S Q L V E T A L L A L G
316 tattcccacagctctgcagcgcaggcccaaggaataatcaagcta
Y S H S S A A Q A Q G I I K L
361 gggaggtggaacccccctccccctcagttatgtgacagacgcccct
G R W N P L P L S Y V T D A P
406 gatgcgactgtggccgacatgctgcaagatgtctatcacgtttgtg
D A T V A D M L Q D V Y H V V
451 acgctgaagatccaattacaaagtgttcaaagttggaagacttg
T L K I Q L Q S C S K L E D L
496 cctgcggagcaatggaaccacgccaccgtccgcaatgccttaaag
P A E Q W N H A T V R N A L K
541 gaactgctcaaagaaatgaaccagagcacattagccaaagaatgc
E L L K E M N Q S T L A K E C
586 cctctctcccagagtatgatttcatccattgtaaatagcacatac
P L S Q S M I S S I V N S T Y
631 tatgccaatgtgtcagcaaccaagtgccaggagtttgggagatgg
Y A N V S A T K C Q E F G R W
676 tacaaaaagtataagaagataaaagtggaaagagtggagcgagag
Y K K Y K K I K V E R V E R E
721 aacctttcagactattgtgttcttgggccagcggccaatgcattta
N L S D Y C V L G Q R P M H L
766 ccaaatatgaaccagctggcatccctgggcaaaaccaacgaacag
P N M N Q L A S L G K T N E Q
811 tctcctcatagccaaatccaccacagtactccaatccgaaaccaa
S P H S Q I H H S T P I R N Q
856 gtgcccgcactccagcccatcatgagccctggtcttctctcaccg
V P A L Q P I M S P G L L S P
901 cagctcagtcctcagcttgtcaggcagcaaataagccatggcccat
Q L S P Q L V R Q Q I A M A H
946 ctgataaaaccaacagatagccgttagccgactcctgggtcaccag
L I N Q Q I A V S R L L A H Q
991 catcctcaagccatcaaccagcagttcttgaaccacccaccatt
H P Q A I N Q Q F L N H P P I

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1036 cccagagcagttaagccagagccaacaaactcctctgtggaagtc
P R A V K P E P T N S S V E V
1081 tctcctgatatctaccagcaagtttagagatgagttgaagagggt
S P D I Y Q Q V R D E L K R A
1126 agtgtgtctcaagctgtctttgcaagagtggcattcaaccgcaca
S V S Q A V F A R V A F N R T
1171 cagggattattgtcagagatactgcgtaaggaagaagatcccagg
Q G L L S E I L R K E E D P R
1216 actgctgtcagtcctcttctagtaaactgagggccatgcagaac
T A S Q S L L V N L R A M Q N
1261 ttcctcaacctgcctgaagtggagcgtgatcgcatttaccaggat
F L N L P E V E R D R I Y Q D
1306 gagcgagagaggagcatgaaccccaatgtgagcatggtctcctct
E R E R S M N P N V S M V S S
1351 gcctctagcagtcctcagctcctccgaacccacaggccaaaacc
A S S S P S S S R T P Q A K T
1396 tcgacaccgacaacagacctccctattaaggtggacggcgccaac
S T P T T D L P I K V D G A N
1441 gtcaacatcacagctgccatttatgacgagatccaacaggagatg
V N I T A A I Y D E I Q Q E M
1486 aaaagagccaaggtgtctcaagccctgtttgccaaagtggctgca
K R A K V S Q A L F A K V A A
1531 aacaaaagtcagggctggctttggaactgcttcgttggaaggag
N K S Q G W L C E L L R W K E
1576 aaccccagcccagaaaaaccgcaccctttgggagaatctctgcacc
N P S P E N R T L W E N L C T
1621 atccgccgtttcctgaatcttccccaacatgagcgggatgtgatc
I R R F L N L P Q H E R D V I
1666 tatgaggaagaatctcgacatcaccacagtgaaacgcagcagcat
Y E E E S R H H H S E R M Q H
1711 gtggtccagctcccacctgagcccggtgcaggtccttcacgcagac
V V Q L P P E P V Q V L H R Q
1756 cagtcccagccaactaaggagagctcccctcccagagaagaagca
Q S Q P T K E S S P P R E E A
1801 cccccaccgcctcctccaacagaagacagctgtgccccaaaagcct
P P P P P P T E D S C A K K P
1846 cggctctcgacaaaagatctctttggaagccctgggcacatccttcaa
R S R T K I S L E A L G I L Q
1891 agcttcatccatgatgtaggcctctatcccagaccaggaagccatc
S F I H D V G L Y P D Q E A I
1936 cacacactctccgcccagctggatctcccaaacacaccatcatc
H T L S A Q L D L P K H T I I
1981 aagttcttccagaaccagaggtaccacgtgaagcaccacgggaag
K F F Q N Q R Y H V K H H G K
2026 ctgaaagagcacctgggctccgcggtggacgtggctgaatataag
L K E H L G S A V D V A E Y K
2071 gacgaggagctgctgaccgagtcagaggagaacgacagcgaggaa
D E E L L T E S E E N D S E E
2116 ggctccgaggagatgtacaaagtggaggctgaggaggaaaatgct
G S E E M Y K V E A E E E N A
2161 gacaaaagcaaggcagcacctgccgaaattgaccagagataa 2202
D K S K A A P A E I D Q R *

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FIGURE 9 SEQ ID NO:4 Mouse protein sequence

001	MERRSESPCL	RDSPDRRSGS	PDVKGPPPVK	VARLEQNGSP	MGARGRPNGA
051	VAKAVGGLMI	PVFCVVEQLD	GSLEYDNREE	HAEFVLVRKD	VLFSQLVETA
101	LLALGYSHSS	AAQAQGIIKL	GRWNPLPLSY	VTDAPDATVA	DMLQDVYHVV
151	TLKIQLOSCS	KLEDLPAEQW	NHATVRNALK	ELLKEMNQST	LAKECPLSQS
201	MISSIVNSTY	YANVSATKCQ	EFGRWYKKYK	KIKVERVERE	NLSDYCVLGQ
251	RPMHLPNMNQ	LASLGKTNEQ	SPHSQIHHST	PIRNQVPALQ	PIMSPGLLSP
301	QLSPQLVRQQ	IAMAHLINQQ	IAVSRLLAHQ	HPQAINQQFL	NHPPIPRAVK
351	PEPTNSSVEV	SPDIYQQVRD	ELKRASVSQA	VFARVAFNRT	QGLLSEILRK
401	EEDPRTASQS	LLVNLRAMQN	FLNLPEVERD	RIYQDERERS	MNPNVSMVSS
451	ASSSPSSSRT	PQAKTSTPTT	DLPIKVDGAN	VNITAAIYDE	IQQEMKRAKV
501	SQALFAKVAA	NKSQGWLCLE	LRWKENPSPE	NRTLWENLCT	IRRFLNLPQH
551	ERDVIYEEES	RHHHSERMQH	VVQLPPEPVQ	VLHRQQSQPT	KESSPPREEA
601	PPPPPTEDS	CAKKPRSRTK	ISLEALGILQ	SFIHDVGLYP	DQEAHTLSA
651	QLDLPKHTII	KFFQNQRYHV	KHHGKLKEHL	GSAVDVAEYK	DEELLTESEE
701	NDSEEGSEEM	YKVEAEEENA	DKSKAAPAEI	DQR	

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TABLE 1: Oligonucleotides used in the Study.

Marker	Oligonucleotide Primers	YACs isolated	Chimeric by FISH	SEQ ID NO
D2S311	dCAATTTTGAGCCCGGAAG	17GD1	+	5
	dTGACTAGAAAGGCATTCCAGAG	31CH5	-	6
		33AC9	-	
D2S115	dCAAGAACAGCCATATTGACTTGAAC	11GG8	-	7
	dGGGTACAGCCCATGTGTGAG			8
D2S348	dAGGTGACCAGCAGCCTCT	19ID10	ND	9
	dGTAAACGGACATATCCCCC	21GA12	ND	10
		23EG11	ND	
		32EB9	ND	
D2S72	dAGCTATAATTGCATCATTGCA	26IF5	-	11
	dTGGTCTATAACGGTCTATG			12
D2S105	dCTCTACAGTTTATAACCAGC	26IF5	-	13
	dTACACTGGATTCATATTCCC			14
C7LA4	dATTTCAATTTCCAAGAGCTGAGG	26IF5	-	15
	dGCTGATGTGACAGAAACATCCC	8IH5	ND	16
		13HC12	ND	
		20AG2	ND	
		22HB6	ND	
D2S307	dCATGACCTGAAATAAACATAGACA	26IF5	-	17
	dDAGCTTTTCCTGTAGGCTGTC	22HB6	ND	18
		6BC7	ND	
D2S1384	dAATAGAGGGCCCTTGCTTAA	26IF5	-	19
	dTTTGGGATAAAAGGTATTTTGC	22HB6	ND	20
		10GF2	ND	
W15293	dGAGTTAGACCCCGTCTAAAAAAA	26IF5	-	21
	dACTCTCATCTCCTTCCTTGTTC	8BG7	ND	22
		14HA2	-	
		24GF8	ND	
D2S2189	dTACAAAAGGACTTGTCCAGGG	8BG7	ND	23
	dTCAAGATTGCCGTGAGGT	14HAZ	-	24

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		23CE7	ND	
		24GF8	ND	
D2S1271	dGGAAGGTCCAGATTAGAAG	15BA12	ND	25
	dAAGGGAAATAAAGAGAAGCAT	22HC8	ND	26
D2S116	dCAATCTCCACAAGTTGCTCA	6HA11	-	27
	dGGGATAGATAATTTAGGAGTGGG	13BE7	ND	28
		14DE4	ND	
		16IB4	+	
		28DE5	ND	
D2S309	dGCTCTAGTAGGCTGGTTACATAA	4EC12	+	29
	dTTCCAAGAATAATGCAATCTCAG	31DH5	+	30
<i>FNI</i>	dTTGTTCCTACAGTATTGCGGG	7AH3	+	31
	dCCAACCCAAGATGCAAATG	11GH11	ND	32
		31GG9	-	
		37HB8	ND	
<i>IGFBP5</i>	dCTATTGGGGTTTCCCAGGAT	21EC3	-	33
	dTTTCCAATATTGGGGCATGT	22DB10	ND	34
<i>IGFBP2</i>	dCAGTAGACCGCAGCCAGC	7FA11	ND	35
	dGGAAAGCAAGAAGGAGCAGG	8HF12	ND	36
		21EC3	-	
		22DB10	ND	
<i>IHH</i>	dGGACTCCACCTGGAAGTGC	35EF10	-	37
	dGAAAACCTCGTAGTGAGAGCAG			38

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TABLE 2: Genetic Map of CP-1 Region

A	Cen	B	Cen	
	D2S311		D2S311	der (2)
			D2S374	⇐
			D2S1413	⇐
	D2S2327		D2S115	der (7) / der (11)
			D2S348	der (7) / der (11)
	D2S2396		D2S72	der (7) / der (11)
			(D2S2327)	
	D2S374		(D2S2396)	
	D2S2217		D2S105	der (7) / der (11)
			CTLA4	der (7) / der (11)
	1.4cM		D2S307	der (7) / der (11)
			(D2S2217)	
	D2S2392		(D2S2392)	
			(D2S1740)	
	0.1			
	cM		(D2S2708)	
			(D2S1837)	
	D2S309		(D2S2684)	
			(D2S1367)	
	Tel		D2S1384	der (7) / der (11)
			WIS293	der (7) / der (11)
			D2S2189	der (7) / der (11)
			D2S1271	der (7) / der (11)
			D2S116	der (7) / der (11)
			D2S309	der (7) / der (11)
			Tel	